STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: _10/533,104_

Source: _Pat/io_

Date Processed by STIC: _5/10/05_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
       http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission
   User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
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   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street,
   Alexandria, VA 22314

Revised 01/24/05

Suggestion: Consult Sequence Rules

PCT

delete this
show <110> only once

RAW SEQUENCE LISTING   DATE: 05/10/2005
PATENT APPLICATION: US/10/533,104   TIME: 13:45:04

Input Set : N:\DA\PTO.DA.txt
Output Set: N:\CRF4\05102005\J533104.raw

```
       2 <110> APPLICANT: Chugai Seiyaku Kabushiki Kaisha
W-->   3 <110> APPLICANT: University College London
W-->   4 <120> TITLE OF INVENTION: HM 1.24-UTILIZING CANCER VACCINES
W-->   5 <130> FILE REFERENCE: M915
C-->   6 <140> CURRENT APPLICATION NUMBER: US/10/533,104
C-->   6 <141> CURRENT FILING DATE: 2005-04-28
E-->   6 <160> NUMBER OF SEQ ID NOS:
```

23 (see p.5)

→ mandatory
response needed

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

```
      41 <210> SEQ ID NO: 5
      42 <211> LENGTH: 396
      43 <212> TYPE: DNA
      44 <213> ORGANISM: Homosapiens
```

insert
<2207 wherever <2217, <2227, or <2237 is shown

```
      45 <223> OTHER INFORMATION: Nucleotide sequence of extracellular domain of soluble HM
1.24 antigenic
      46       protein
      47 <400> SEQUENCE: 5
      48 aac agc gag gcc tgc cgg gac ggc ctt cgg gca gtg atg gag tgt cgc        48
      49 Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg
      50   1               5                  10                  15
      51 aat gtc acc cat ctc ctg caa caa gag ctg acc gag gcc cag aag ggc        96
      52 Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly
      53              20                  25                  30
      54 ttt cag gat gtg gag gcc cag gcc gcc acc tgc aac cac act gtg atg       144
      55 Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met
      56          35                  40                  45
      57 gcc cta atg gct tcc ctg gat gca gag aag gcc caa gga caa aag aaa       192
      58 Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys
      59      50                  55                  60
      60 gtg gag gag ctt gag gga gag atc act aca tta aac cat aag ctt cag       240
      61 Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln
      62   65                  70                  75                  80
      63 gac gcg tct gca gag gtg gag cga ctg aga aga gaa aac cag gtc tta       288
      64 Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu
      65                  85                  90                  95
      66 agc gtg aga atc gcg gac aag aag tac tac ccc agc tcc cag gac tcc       336
      67 Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser
      68             100                 105                 110
      69 agc tcc gct gcg gcg ccc cag ctg ctg att gtg ctg ctg ggc ctc agc       384
      70 Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser
      71             115                 120                 125
      72 gct ctg ctg cag                                                       396
```

```
 73 Ala Leu Leu Gln
 74       130
 83 <210> SEQ ID NO: 7
 84 <211> LENGTH: 345
 85 <212> TYPE: DNA                        insert
 86 <213> ORGANISM: Homosapiens        <220>
 87 <223> OTHER INFORMATION: Nucleotide sequence of extracellular domain of C-terminal-
lacking soluble
 88       HM 1.24 antigenic protein
 89 <400> SEQUENCE: 7
 90 aac agc gag gcc tgc cgg gac ggc ctt cgg gca gtg atg gag tgt cgc      48
 91 Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg
 92  1           5                   10                  15
 93 aat gtc acc cat ctc ctg caa caa gag ctg acc gag gcc cag aag ggc      96
 94 Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly
 95          20                  25                  30
 96 ttt cag gat gtg gag gcc cag gcc gcc acc tgc aac cac act gtg atg     144
 97 Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met
 98          35                  40                  45
 99 gcc cta atg gct tcc ctg gat gca gag aag gcc caa gga caa aag aaa     192
100 Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys
101       50                  55                  60
102 gtg gag gag ctt gag gga gag atc act aca tta aac cat aag ctt cag     240
103 Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln
104  65              70                  75                  80
105 gac gcg tct gca gag gtg gag cga ctg aga aga gaa aac cag gtc tta     288
106 Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu
107               85                  90                  95
108 agc gtg aga atc gcg gac aag aag tac tac ccc agc tcc cag gac tcc     336
109 Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser
110               100                 105                 110
111 agc tcc gct                                                        345
112 Ser Ser Ala
113          115
165 <210> SEQ ID NO: 11
166 <211> LENGTH: 378
167 <212> TYPE: DNA
168 <213> ORGANISM: Artificial Sequence
169 <220>  <- insert
169 <223> OTHER INFORMATION: Nucleotide sequence coding for a fusion protein comprising
HA peptide and
170       C-terminal- lacking soluble HM 1.24 antigenic protein
171 <400> SEQUENCE: 11
172 tac cca tac gac gtc cca gac tac gct ggt acc aac agc gag gcc tgc      48
173 Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Thr Asn Ser Glu Ala Cys
174  1           5                   10                  15
175 cgg gac ggc ctt cgg gca gtg atg gag tgt cgc aat gtc acc cat ctc      96
176 Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu
177          20                  25                  30
178 ctg caa caa gag ctg acc gag gcc cag aag ggc ttt cag gat gtg gag     144
179 Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu
```

RAW SEQUENCE LISTING   DATE: 05/10/2005
PATENT APPLICATION: US/10/533,104   TIME: 13:45:04

Input Set : **N:\DA\PTO.DA.txt**
Output Set: **N:\CRF4\05102005\J533104.raw**

```
180          35                      40                       45
181 gcc cag gcc gcc acc tgc aac cac act gtg atg gcc cta atg gct tcc    192
182 Ala Gln Ala Ala Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser
183          50                      55                      60
184 ctg gat gca gag aag gcc caa gga caa aag aaa gtg gag gag ctt gag    240
185 Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu
186   65                      70                      75              80
187 gga gag atc act aca tta aac cat aag ctt cag gac gcg tct gca gag    288
188 Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu
189                  85                      90                      95
190 gtg gag cga ctg aga aga gaa aac cag gtc tta agc gtg aga atc gcg    336
191 Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala
192              100                     105                   110
193 gac aag aag tac tac ccc agc tcc cag gac tcc agc tcc gct            378
194 Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala
195          115                     120                     125
298 <210> SEQ ID NO: 15
299 <211> LENGTH: 1014
300 <212> TYPE: DNA
301 <213> ORGANISM: Homosapiens            <220>
302 <223> OTHER INFORMATION: Nucleotide sequence coding for (humam) HM 1.24 antigenic
protein expressed
303          on cell membrane
304 <400> SEQUENCE: 15
305 gaattcggca cgagggatct gg atg gca tct act tcg tat gac tat tgc       49
306                        Met Ala Ser Thr Ser Tyr Asp Tyr Cys
307                         1               5
308 aga gtg ccc atg gaa gac ggg gat aag cgc tgt aag ctt ctg ctg ggg    97
309 Arg Val Pro Met Glu Asp Gly Asp Lys Arg Cys Lys Leu Leu Leu Gly
310  10                     15                      20                      25
311 ata gga att ctg gtg ctc ctg atc atc gtg att ctg ggg gtg ccc ttg    145
312 Ile Gly Ile Leu Val Leu Leu Ile Ile Val Ile Leu Gly Val Pro Leu
313                  30                      35                      40
314 att atc ttc acc atc aag gcc aac agc gag gcc tgc cgg gac ggc ctt    193
315 Ile Ile Phe Thr Ile Lys Ala Asn Ser Glu Ala Cys Arg Asp Gly Leu
316              45                      50                      55
317 cgg gca gtg atg gag tgt cgc aat gtc acc cat ctc ctg caa caa gag    241
318 Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu Leu Gln Gln Glu
319              60                      65                      70
320 ctg acc gag gcc cag aag ggc ttt cag gat gtg gag gcc cag gcc gcc    289
321 Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu Ala Gln Ala Ala
322          75                      80                      85
323 acc tgc aac cac act gtg atg gcc cta atg gct tcc ctg gat gca gag    337
324 Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser Leu Asp Ala Glu
325   90                      95                      100                     105
326 aag gcc caa gga caa aag aaa gtg gag gag ctt gag gga gag atc act    385
327 Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu Gly Glu Ile thr
328                  110                     115                     120
329 aca tta aac cat aag ctt cag gac gcg tct gca gag gtg gag cga ctg    433
330 Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu Val Glu Arg Leu
```

human?

RAW SEQUENCE LISTING   DATE: 05/10/2005
PATENT APPLICATION: US/10/533,104   TIME: 13:45:04

Input Set : N:\DA\PTO.DA.txt
Output Set: N:\CRF4\05102005\J533104.raw

```
331              125                130                135
332 aga aga gaa aac cag gtc tta agc gtg aga atc gcg gac aag aag tac    481
333 Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala Asp Lys Lys Tyr
334          140                145                150
335 tac ccc agc tcc cag gac tcc agc tcc gct gcg gcg ccc cag ctg ctg    529
336 Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala Ala Ala Pro Gln Leu Leu
337       155                160                165
338 att gtg ctg ctg ggc ctc agc gct ctg ctg cag tgagatccca ggaagctggc  582
339 Ile Val Leu Leu Gly Leu Ser Ala Leu Leu Gln
340 170                175                180
341 acatcttgga aggtccgtcc tgctcggctt ttcgcttgaa cattcccttg atctcatcag   642
342 ttctgagcgg gtcatggggc aacacggtta gcggggagag cacggggtag ccggagaagg   702
343 gcctctggag caggtctgga ggggccatgg ggcagtcctg ggtgtgggga cacagtcggg   762
344 ttgacccagg gctgtctccc tccagagcct ccctccggac aatgagtccc ccctcttgtc   822
345 tcccaccctg agattgggca tggggtgcgg tgtggggggc atgtgctgcc tgttgttatg   882
346 ggtttttttt gcggggggg ttgctttttt ctggggtctt tgagctccaa aaaaataaac    942
347 acttcctttg agggagagca caccttaaaa aaaaaaaaaa aaaaaaaaaa aaaaaattc    1002
348 gggcggccgc ca                                                       1014
349 <210> SEQ ID NO: 16
350 <211> LENGTH: 132
351 <212> TYPE: PRT
352 <213> ORGANISM: Homosapiens    insert <220>
353 <223> OTHER INFORMATION: Amino acid sequence of soluble HM 1.24 antigenic protein
354 <400> SEQUENCE: 16
355 Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg
356  1              5                10                15
357 Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly
358          20                25                30
359 Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met
360          35                40                45
361 Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys
362       50                55                60
363 Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln
364  65                70                75                80
365 Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu
366          85                90                95
367 Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser
368          100                105                110
369 Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser
370          115                120                125
371 Ala Leu Leu Gln
372       130
373 <210> SEQ ID NO: 17
374 <211> LENGTH: 115
375 <212> TYPE: PRT
376 <213> ORGANISM: Homosapiens    insert <220>
377 <223> OTHER INFORMATION: Amino acid sequence of extra cellular downing of C-terminal
lacking
378       soluble HM 1.24 antigenic protein
379 <400> SEQUENCE: 17
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/533,104

DATE: 05/10/2005
TIME: 13:45:04

Input Set : N:\DA\PTO.DA.txt
Output Set: N:\CRF4\05102005\J533104.raw

```
380 Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg
381  1               5                   10                  15
382 Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly
383             20                  25                  30
384 Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met
385             35                  40                  45
386 Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys
387         50                  55                  60
388 Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln
389  65                  70                  75                  80
390 Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu
391             85                  90                  95
392 Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser
393             100                 105                 110
394 Ser Ser Ala
395         115
522 <210> SEQ ID NO: 23
523 <211> LENGTH: 180
524 <212> TYPE: PRT
525 <213> ORGANISM: Homosapiens
526 <223> OTHER INFORMATION: Amino acid sequence of humam HM 1.24 antigenic protein
expressed on cell
527         membrane
528 <400> SEQUENCE: 23
529 Met Ala Ser Thr Ser Tyr Asp Tyr Cys Arg Val Pro Met Glu Asp Gly
530  1               5                   10                  15
531 Asp Lys Arg Cys Lys Leu Leu Leu Gly Ile Gly Ile Leu Val Leu Leu
532             20                  25                  30
533 Ile Ile Val Ile Leu Gly Val Pro Leu Ile Ile Phe Thr Ile Lys Ala
534             35                  40                  45
535 Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg
536         50                  55                  60
537 Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly
538  65                  70                  75                  80
539 Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met
540             85                  90                  95
541 Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys
542             100                 105                 110
543 Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln
544         115                 120                 125
545 Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu
546     130                 135                 140
547 Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser
548 145                 150                 155                 160
549 Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser
550             165                 170                 175
551 Ala Leu Leu Gln
552         180
```

last sequence in submitted file → *insert* ⟨220⟩ human?

(humam) circled

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 05/10/2005
PATENT APPLICATION: **US/10/533,104**   TIME: 13:45:05

Input Set : **N:\DA\PTO.DA.txt**
Output Set: **N:\CRF4\05102005\J533104.raw**

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:7; Line(s) 87
Seq#:10; Line(s) 135
Seq#:11; Line(s) 169
Seq#:18; Line(s) 401

```
<210> 1
<211> 109
<212> DNA
<213> Artificial Sequence        ⟩ I believe this goes on <160> line.
<220> (23)
<223> Synthetic DNA comprising leader sequence and HA coding sequence
<400> 1
```

VERIFICATION SUMMARY   DATE: 05/10/2005
PATENT APPLICATION: **US/10/533,104**   TIME: 13:45:05

Input Set : **N:\DA\PTO.DA.txt**
Output Set: **N:\CRF4\05102005\J533104.raw**

L:3 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:4 M:283 W: Missing Blank Line separator, <120> field identifier
L:5 M:283 W: Missing Blank Line separator, <130> field identifier
L:6 M:270 C: Current Application Number differs, Replaced Current Application No
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:6 M:212 E: (34) Invalid or duplicate Sequence ID Number, Number Of Sequences Unknown
L:6 M:283 W: Missing Blank Line separator, <160> field identifier
L:7 M:283 W: Missing Blank Line separator, <210> field identifier
L:11 M:283 W: Missing Blank Line separator, <220> field identifier
L:11 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:13 M:283 W: Missing Blank Line separator, <400> field identifier
L:20 M:283 W: Missing Blank Line separator, <220> field identifier
L:22 M:283 W: Missing Blank Line separator, <400> field identifier
L:29 M:283 W: Missing Blank Line separator, <220> field identifier
L:31 M:283 W: Missing Blank Line separator, <400> field identifier
L:37 M:283 W: Missing Blank Line separator, <220> field identifier
L:39 M:283 W: Missing Blank Line separator, <400> field identifier
L:47 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:5
L:47 M:283 W: Missing Blank Line separator, <400> field identifier
L:79 M:283 W: Missing Blank Line separator, <220> field identifier
L:81 M:283 W: Missing Blank Line separator, <400> field identifier
L:89 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:7
L:89 M:283 W: Missing Blank Line separator, <400> field identifier
L:118 M:283 W: Missing Blank Line separator, <220> field identifier
L:120 M:283 W: Missing Blank Line separator, <400> field identifier
L:126 M:283 W: Missing Blank Line separator, <220> field identifier
L:128 M:283 W: Missing Blank Line separator, <400> field identifier
L:134 M:283 W: Missing Blank Line separator, <220> field identifier
L:137 M:283 W: Missing Blank Line separator, <400> field identifier
L:169 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:171 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:11
L:171 M:283 W: Missing Blank Line separator, <400> field identifier
L:200 M:283 W: Missing Blank Line separator, <220> field identifier
L:203 M:283 W: Missing Blank Line separator, <400> field identifier
L:232 M:283 W: Missing Blank Line separator, <220> field identifier
L:235 M:283 W: Missing Blank Line separator, <400> field identifier
L:267 M:283 W: Missing Blank Line separator, <220> field identifier
L:270 M:283 W: Missing Blank Line separator, <400> field identifier
L:304 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:15
L:304 M:283 W: Missing Blank Line separator, <400> field identifier
L:354 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:16
L:354 M:283 W: Missing Blank Line separator, <400> field identifier
L:379 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:17
L:379 M:283 W: Missing Blank Line separator, <400> field identifier
L:400 M:283 W: Missing Blank Line separator, <220> field identifier
L:403 M:283 W: Missing Blank Line separator, <400> field identifier
L:426 M:283 W: Missing Blank Line separator, <220> field identifier
L:429 M:283 W: Missing Blank Line separator, <400> field identifier

```
L:450 M:283 W: Missing Blank Line separator, <220> field identifier
L:453 M:283 W: Missing Blank Line separator, <400> field identifier
L:474 M:283 W: Missing Blank Line separator, <220> field identifier
L:477 M:283 W: Missing Blank Line separator, <400> field identifier
L:500 M:283 W: Missing Blank Line separator, <220> field identifier
L:503 M:283 W: Missing Blank Line separator, <400> field identifier
L:528 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:23
L:528 M:283 W: Missing Blank Line separator, <400> field identifier
L:6 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (0) Counted (23)
```